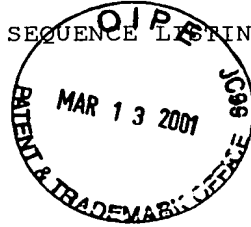


SEQUENCE LISTING



<110> YAMAMOTO, Takuo
MARUTA, Kazuhiko
KUBOTA, Michio
FUKUDA, Shigeharu
MIYAKE, Toshio

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TREHALOSE-RELEASING ENZYME, AND PROCESS FOR PRODUCING
SACCHARIDES USING THE ENZYMES

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<140> 09/435,770

<141> 1999-11-08

<150> JP 258,394/1998

<151> 1998-09-11

<150> JP 352,252/1998

<151> 1998-12-11

<150> JP 16,931/1999

<151> 1999-01-26

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Glu Gly Leu Ala Glu Leu Ser Arg Ala Ala His Glu Arg Gly Met Gly
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Glu Leu Ala Gln Gly Arg Pro Ile Trp Val Glu Lys Ile Ile Glu Gly	
255 260 265	
gac gag cgg atg ccc ccg cag tgg ccc atc gcc ggc acc acc ggc tac	1588
Asp Glu Arg Met Pro Pro Gln Trp Pro Ile Ala Gly Thr Thr Gly Tyr	
270 275 280	
gac gcg ctg gcc ggg atc gac cgg gtg ctc gtc gac ccc gcg ggc gag	1636
Asp Ala Leu Ala Gly Ile Asp Arg Val Leu Val Asp Pro Ala Gly Glu	
285 290 295	
cat ccg ctc acc cag atc gtc gac gag gcg gca ggc agc ccc cgg cgc	1684
His Pro Leu Thr Gln Ile Val Asp Glu Ala Ala Gly Ser Pro Arg Arg	
300 305 310	
tgg gcc gag ctg gtt ccc gag cgc aag ccg gcc gtc gcc cgc ggc atc	1732
Trp Ala Glu Leu Val Pro Glu Arg Lys Arg Ala Val Ala Arg Gly Ile	
315 320 325 330	
ctg aac tcc gag atc cgc cgc gtc gcc cgc gaa ctc gga gag gtc gcc	1780
Leu Asn Ser Glu Ile Arg Arg Val Ala Arg Glu Leu Gly Glu Val Ala	
335 340 345	
ggc gac gtc gaa gac gcg ctc gtc gag atc gcc gcc gcc ctg tcc gtc	1828
Gly Asp Val Glu Asp Ala Leu Val Glu Ile Ala Ala Ala Leu Ser Val	
350 355 360	
tac cgc agc tac ctg ccg ttc ggg cgc gag cac ctc gac gaa gcc gtg	1876
Tyr Arg Ser Tyr Leu Pro Phe Gly Arg Glu His Leu Asp Glu Ala Val	
365 370 375	
gcc gcc gcg cag gcc gca gcc ccc cag ctc gag gcc gac ctc gcc gcc	1924
Ala Ala Ala Gln Ala Ala Ala Pro Gln Leu Glu Ala Asp Leu Ala Ala	
380 385 390	
gtc ggc gca gcg ctc gcc gac ccg ggc aac ccc gcc gcg ctc cgc ttc	1972
Val Gly Ala Ala Leu Ala Asp Pro Gly Asn Pro Ala Ala Leu Arg Phe	
395 400 405 410	
cag cag acc agc ggc atg atc atg gcc aag ggc gtc gag gac aac gcg	2020

B1

Gln	Gln	Thr	Ser	Gly	Met	Ile	Met	Ala	Lys	Gly	Val	Glu	Asp	Asn	Ala		
				415					420					425			
ttc	tac	cgc	tac	ccc	cgg	ctc	acc	tcg	ctg	acc	gag	gtc	ggg	gga	gac		2068
Phe	Tyr	Arg	Tyr	Pro	Arg	Leu	Thr	Ser	Leu	Thr	Glu	Val	Gly	Gly	Asp		
			430					435					440				
ccg	agc	ctg	ttc	gcg	atc	gac	gcg	gcc	gcc	ttc	cac	gcg	gcg	cag	cgc		2116
Pro	Ser	Leu	Phe	Ala	Ile	Asp	Ala	Ala	Ala	Phe	His	Ala	Ala	Gln	Arg		
		445					450					455					
gac	cgc	gcc	gcc	cgg	ctg	ccc	gag	tcg	atg	acg	acg	ctg	acc	acc	cac		2164
Asp	Arg	Ala	Ala	Arg	Leu	Pro	Glu	Ser	Met	Thr	Thr	Leu	Thr	Thr	His		
	460					465				470							
gac	acc	aag	cgc	agc	gaa	gac	acc	cgg	gcg	cgg	atc	acc	gcg	ctc	gcc		2212
Asp	Thr	Lys	Arg	Ser	Glu	Asp	Thr	Arg	Ala	Arg	Ile	Thr	Ala	Leu	Ala		
	475				480					485					490		
gag	gcc	ccc	gaa	cgc	tgg	cgg	cgc	ttc	ctg	acc	gag	gtc	ggc	ggg	ctc		2260
Glu	Ala	Pro	Glu	Arg	Trp	Arg	Arg	Phe	Leu	Thr	Glu	Val	Gly	Gly	Leu		
				495				500						505			
atc	gga	acg	ggc	gac	cgg	gtg	ctg	gag	aac	ctg	atc	tgg	cag	gcg	atc		2308
Ile	Gly	Thr	Gly	Asp	Arg	Val	Leu	Glu	Asn	Leu	Ile	Trp	Gln	Ala	Ile		
			510					515					520				
gtc	ggc	gcg	tgg	ccg	gcg	agc	cgg	gag	cgg	ctc	gag	gcc	tac	gcg	ctg		2356
Val	Gly	Ala	Trp	Pro	Ala	Ser	Arg	Glu	Arg	Leu	Glu	Ala	Tyr	Ala	Leu		
		525					530					535					
aag	gcc	gcg	cgc	gaa	gcc	ggc	gag	tcg	acc	gac	tgg	atc	gac	ggc	gac		2404
Lys	Ala	Ala	Arg	Glu	Ala	Gly	Glu	Ser	Thr	Asp	Trp	Ile	Asp	Gly	Asp		
	540					545					550						
ccc	gcg	ttc	gaa	gag	cgg	ctg	acc	cgc	ctg	gtc	acg	gtc	gcc	gtc	gag		2452
Pro	Ala	Phe	Glu	Glu	Arg	Leu	Thr	Arg	Leu	Val	Thr	Val	Ala	Val	Glu		
	555				560					565					570		
gag	ccg	ctc	gtg	cac	gag	ctg	ctc	gag	cgg	ctc	gtc	gac	gag	ctg	acg		2500
Glu	Pro	Leu	Val	His	Glu	Leu	Leu	Glu	Arg	Leu	Val	Asp	Glu	Leu	Thr		
				575					580					585			
gcg	gcc	ggg	tac	tcc	aac	ggc	ctc	gcg	gcg	aag	ctg	ctg	cag	ctg	ctc		2548
Ala	Ala	Gly	Tyr	Ser	Asn	Gly	Leu	Ala	Ala	Lys	Leu	Leu	Gln	Leu	Leu		
			590					595					600				
gcc	ccc	gga	acc	ccc	gac	gtg	tac	cag	ggc	acg	gaa	cgc	tgg	gac	cgg		2596
Ala	Pro	Gly	Thr	Pro	Asp	Val	Tyr	Gln	Gly	Thr	Glu	Arg	Trp	Asp	Arg		
		605				610						615					
tcg	ctg	gtg	gac	ccg	gac	aac	cgt	cgc	ccc	gtg	gat	ttc	gcc	gcg	gca		2644
Ser	Leu	Val	Asp	Pro	Asp	Asn	Arg	Arg	Pro	Val	Asp	Phe	Ala	Ala	Ala		
	620					625					630						
tcc	gag	ctg	ctc	gac	cgc	ctc	gac	ggc	ggc	tgg	cgg	ccg	ccc	gtc	gac		2692
Ser	Glu	Leu	Leu	Asp	Arg	Leu	Asp	Gly	Gly	Trp	Arg	Pro	Pro	Val	Asp		
	635				640					645				650			
gag	acc	ggc	gcg	gtc	aag	acg	ctc	gtc	gtc	tcc	cgc	gcg	ctg	cgg	ctg		2740
Glu	Thr	Gly	Ala	Val	Lys	Thr	Leu	Val	Val	Ser	Arg	Ala	Leu	Arg	Leu		

655	660	665	
cgc cgc gac cgg ccc gag ctg ttc acc gcg tac cac ccg gtc acg gcg			2788
Arg Arg Asp Arg Pro Glu Leu Phe Thr Ala Tyr His Pro Val Thr Ala			
670	675	680	
cgc ggc gcg cag gcc gag cac ctg atc ggc ttc gac cgc ggc ggc gcg			2836
Arg Gly Ala Gln Ala Glu His Leu Ile Gly Phe Asp Arg Gly Gly Ala			
685	690	695	
atc gcc ctg gcc acc cgc ctg ccg ctc ggc ctc gcc gcc gca ggc ggc			2884
Ile Ala Leu Ala Thr Arg Leu Pro Leu Gly Leu Ala Ala Ala Gly Gly			
700	705	710	
tgg ggc gac acg gtc gtc gac gtc ggc gag cgg agc ctg cgc gac gag			2932
Trp Gly Asp Thr Val Val Asp Val Gly Glu Arg Ser Leu Arg Asp Glu			
715	720	725	730
ctg acc ggc cgc gag gcc cgc gga gcg gcg cgc gtg gcc gag ttg ttc			2980
Leu Thr Gly Arg Glu Ala Arg Gly Ala Ala Arg Val Ala Glu Leu Phe			
735	740	745	
gcc gac tac ccc gtc gcc ctg ctg gtg gag aca tgaaccgacg attcccggtc			3033
Ala Asp Tyr Pro Val Ala Leu Leu Val Glu Thr			
750	755		
tgggcgcccc aggcgcgcga ggtgacgtc gtcgtgggcc aaggccgcgc cgaactcccg			3093
ctgaccgcgcg acgagaacgg atggtgggct cttcagcagc cgtgggacgg cggccccgac			3153
ctcgtcgact acggctacct cgtcgacggc aagggcccct tcgccgaccc gcggtcgctg			3213
cggcagccgc gcggcgtgca cgagctcggc cgcaattc			3252

<210> 20
 <211> 26
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:SYNTHETIC

<400> 20
 atgcccgcca gtacctaccg ccttca 26

<210> 21
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:SYNTHETIC

<400> 21
 tcatgtctcc accagcaggg cgacg 25

<210> 22
 <211> 50
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:SYNTHETIC

 <400> 22
 aattcttttt taataaaatc aggaggaatc tagatgttta ctagtctgca 50

 <210> 23
 <211> 42
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:SYNTHETIC

 <400> 23
 gactagtaaa catctagatt cctcctgatt ttattaaaaa ag 42

 <210> 24
 <211> 33
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:SYNTHETIC

 <400> 24
 aaatctagat gcccgccagt acctaccgcc ttc 33

 <210> 25
 <211> 33
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:SYNTHETIC

 <400> 25
 aaaactagtt tatcatgtct ccaccagcag ggc 33

 <210> 26
 <211> 22
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:SYNTHETIC

 <400> 26
 atcggatgatg tcggcgatat ag 22

 <210> 27
 <211> 29
 <212> DNA
 <213> Artificial Sequence

 <220>

<223> Description of Artificial Sequence:SYNTHETIC

<400> 27

gtactggcgg gcatatTTTT tcctcctga

29

<210> 28

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:SYNTHETIC

<400> 28

aatcaggagg aaaaaatatg cccgccagta c

31

<210> 29

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:SYNTHETIC

<400> 29

tcgacgatct gggtgagcgg at

22

<210> 30

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:SYNTHETIC

<400> 30

tcgacgagca cccggtcgat cc

22

<210> 31

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:SYNTHETIC

<220>

<223> n at position 18 is a, c, g, or t.

<400> 31

cartgggayg aygaygtnc a yca ygc

26

<210> 32

<211> 2218

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:SYNTHETIC

<220>

<221> CDS

<222> (477)..(2201)

<220>

<221> 3'UTR

<222> (2202)..(2218)

<400> 33

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tcgctggtgg acccggaaca cgcgcgcgcg gtggatttcg ccgcggcatc cgagctgctc 120

gaccgcctcg acggcgggctg gcggcgccgc gtcgacgaga ccggcgcggt caagacgctc 180

gtcgtctccc gcgcgctgcg gctgcgcgcg gaccggcccg agctgttcac cgcgtaccac 240

ccgggtcacgg cgcgcggcgc gcaggccgag cacctgatcg gcttcgaccg cggcggcgcg 300

atcgccctgg ccacccgcct gccgctcggc ctgcgcgcg caggcggctg gggcgacacg 360

gtcgtcgacg tcggcgagcg gagcctgcgc gacgagctga ccggccgcga ggcccgcgga 420

gcggcgcgcg tggccgagtt gttcgcccgc taccccgctc ccctgctggt ggagac atg 479

Met

1

aac cga cga ttc ccg gtc tgg gcg ccc cag gcc gcg cag gtg acg ctc 527

Asn Arg Arg Phe Pro Val Trp Ala Pro Gln Ala Ala Gln Val Thr Leu

5

10

15

gtc gtg ggc caa ggc cgc gcc gaa ctc ccg ctg acc cgc gac gag aac 575

Val Val Gly Gln Gly Arg Ala Glu Leu Pro Leu Thr Arg Asp Glu Asn

20

25

30

gga tgg tgg gct ctt cag cag ccg tgg gac ggc ggc ccc gac ctc gtc 623

Gly Trp Trp Ala Leu Gln Gln Pro Trp Asp Gly Gly Pro Asp Leu Val

35

40

45

gac tac ggc tac ctc gtc gac ggc aag ggc ccc ttc gcc gac ccg cgg 671

Asp Tyr Gly Tyr Leu Val Asp Gly Lys Gly Pro Phe Ala Asp Pro Arg

50

55

60

65

tcg ctg cgg cag ccg cgc ggc gtg cac gag ctc ggc cgc gaa ttc gac 719

Ser Leu Arg Gln Pro Arg Gly Val His Glu Leu Gly Arg Glu Phe Asp

70

75

80

ccc gcc cgc tac gcg tgg ggc gac gac gga tgg cgc ggc cga gac ctc 767

Pro Ala Arg Tyr Ala Trp Gly Asp Asp Gly Trp Arg Gly Arg Asp Leu

85

90

95

acc gga gcc gtg atc tac gaa ctg cac gtc ggc acc ttc acc cct gag 815

Thr Gly Ala Val Ile Tyr Glu Leu His Val Gly Thr Phe Thr Pro Glu

100

105

110

gga acg ctg gac agc gcc atc cgt cgc ctc gac cac ctg gtg cgc ctc 863

16137

Gly	Thr	Leu	Asp	Ser	Ala	Ile	Arg	Arg	Leu	Asp	His	Leu	Val	Arg	Leu		
115						120					125						
ggc	gtc	gac	gcg	gtc	gag	ctg	ctg	ccc	gtc	aac	gcg	ttc	aac	ggc	acc	911	
Gly	Val	Asp	Ala	Val	Glu	Leu	Leu	Pro	Val	Asn	Ala	Phe	Asn	Gly	Thr		
130					135					140					145		
cac	ggc	tgg	ggc	tac	gac	ggg	gtg	ctc	tgg	tac	gcg	gtg	cac	gag	ccc	959	
His	Gly	Trp	Gly	Tyr	Asp	Gly	Val	Leu	Trp	Tyr	Ala	Val	His	Glu	Pro		
				150					155					160			
tac	ggc	ggc	ccg	gag	gcg	tac	cag	cgc	ttc	gtc	gac	gcc	tgc	cac	gcc	1007	
Tyr	Gly	Gly	Pro	Glu	Ala	Tyr	Gln	Arg	Phe	Val	Asp	Ala	Cys	His	Ala		
			165					170					175				
cgc	ggc	ctc	gcc	gtc	gtg	cag	gac	gtc	gtc	tac	aac	cac	ctg	ggc	ccg	1055	
Arg	Gly	Leu	Ala	Val	Val	Gln	Asp	Val	Val	Tyr	Asn	His	Leu	Gly	Pro		
		180					185					190					
agc	ggc	aac	cac	ctg	ccc	gac	ttc	ggc	ccc	tac	ctc	ggg	tcg	ggc	gcc	1103	
Ser	Gly	Asn	His	Leu	Pro	Asp	Phe	Gly	Pro	Tyr	Leu	Gly	Ser	Gly	Ala		
	195					200					205						
ggc	aac	acc	tgg	ggc	gac	gcg	ctg	aac	ctc	gac	ggg	ccg	ctc	tcc	gac	1151	
Ala	Asn	Thr	Trp	Gly	Asp	Ala	Leu	Asn	Leu	Asp	Gly	Pro	Leu	Ser	Asp		
210					215					220					225		
gag	gtg	cgg	cgg	tac	atc	atc	gac	aac	gcg	gtg	tac	tgg	ctg	cgc	gac	1199	
Glu	Val	Arg	Arg	Tyr	Ile	Ile	Asp	Asn	Ala	Val	Tyr	Trp	Leu	Arg	Asp		
				230					235					240			
atg	cac	gcc	gac	ggg	ctg	cgg	ctc	gac	gcc	gtg	cac	gcg	ctg	cgc	gac	1247	
Met	His	Ala	Asp	Gly	Leu	Arg	Leu	Asp	Ala	Val	His	Ala	Leu	Arg	Asp		
			245					250					255				
gcc	cgc	gcg	ctg	cac	ctg	ctc	gaa	gag	ctc	gcc	gcc	cgc	gtc	gac	gag	1295	
Ala	Arg	Ala	Leu	His	Leu	Leu	Glu	Glu	Leu	Ala	Ala	Arg	Val	Asp	Glu		
		260					265					270					
ctg	gcg	ggc	gag	ctc	ggc	cgg	ccg	ctg	acg	ctc	atc	gcc	gag	agc	gac	1343	
Leu	Ala	Gly	Glu	Leu	Gly	Arg	Pro	Leu	Thr	Leu	Ile	Ala	Glu	Ser	Asp		
	275					280					285						
ctg	aac	gac	ccg	aag	ctg	atc	cgc	tcc	cgc	gcg	gcg	cac	ggc	tac	ggc	1391	
Leu	Asn	Asp	Pro	Lys	Leu	Ile	Arg	Ser	Arg	Ala	Ala	His	Gly	Tyr	Gly		
290					295				300					305			
ctc	gac	gcc	cag	tgg	gac	gac	gac	gtg	cac	cac	gcg	gtg	cac	gcc	aac	1439	
Leu	Asp	Ala	Gln	Trp	Asp	Asp	Asp	Val	His	His	Ala	Val	His	Ala	Asn		
				310					315					320			
gtg	acc	ggc	gag	acc	gtc	ggc	tac	tac	gcc	gac	ttc	ggc	ggg	ctc	ggc	1487	
Val	Thr	Gly	Glu	Thr	Val	Gly	Tyr	Tyr	Ala	Asp	Phe	Gly	Gly	Leu	Gly		
			325					330					335				
gcc	ctc	gtc	aag	gtg	ttc	cag	cgc	ggc	tgg	ttc	cac	gac	ggc	acc	tgg	1535	
Ala	Leu	Val	Lys	Val	Phe	Gln	Arg	Gly	Trp	Phe	His	Asp	Gly	Thr	Trp		
		340					345					350					
tcg	agc	ttc	cgc	gag	cgg	cac	cac	ggc	cgg	ccg	ctc	gac	ccc	gac	atc	1583	
Ser	Ser	Phe	Arg	Glu	Arg	His	His	Gly	Arg	Pro	Leu	Asp	Pro	Asp	Ile		

355	360	365	
ccg ttc cgc cgg ctc gtc gcc ttc gcg cag gat cac gac cag gtc ggc			1631
Pro Phe Arg Arg Leu Val Ala Phe Ala Gln Asp His Asp Gln Val Gly			
370	375	380	385
aac cga gcg gtc ggc gac cgc atg tcg gcg cag gtc ggc gag ggt tcg			1679
Asn Arg Ala Val Gly Asp Arg Met Ser Ala Gln Val Gly Glu Gly Ser			
	390	395	400
ctc gcc gcc gcg gcg gcg ctc gtg ctg ctc ggc ccg ttc acc ccg atg			1727
Leu Ala Ala Ala Ala Ala Leu Val Leu Leu Gly Pro Phe Thr Pro Met			
	405	410	415
ctg ttc atg ggc gag gag tgg ggc gcg cgc acc ccg tgg cag ttc ttc			1775
Leu Phe Met Gly Glu Glu Trp Gly Ala Arg Thr Pro Trp Gln Phe Phe			
	420	425	430
acc tcc cac ccc gag ccc gag ctg ggg gag gcg acg gcg cgc ggg cgc			1823
Thr Ser His Pro Glu Pro Glu Leu Gly Glu Ala Thr Ala Arg Gly Arg			
	435	440	445
atc gcc gag ttc gcc cgc atg ggc tgg gac ccg gca gtc gtg ccc gac			1871
Ile Ala Glu Phe Ala Arg Met Gly Trp Asp Pro Ala Val Val Pro Asp			
	450	455	460
ccg cag gac ccg gcc acc ttc gcc cgc tcg cac ctg gac tgg tcc gag			1919
Pro Gln Asp Pro Ala Thr Phe Ala Arg Ser His Leu Asp Trp Ser Glu			
	470	475	480
ccc gag cgg gaa ccg cac gcg ggc ctg ctc gcc ttc tac acc gac ctg			1967
Pro Glu Arg Glu Pro His Ala Gly Leu Leu Ala Phe Tyr Thr Asp Leu			
	485	490	495
atc gcg ctg cgg cgc gag ctg ccg gtc gat gcg ccg gcg cgc gag gtg			2015
Ile Ala Leu Arg Arg Glu Leu Pro Val Asp Ala Pro Ala Arg Glu Val			
	500	505	510
gat gcc gac gag gcg cgc ggc gtc ttc gcg ttc agc cgc ggc ccg ctg			2063
Asp Ala Asp Glu Ala Arg Gly Val Phe Ala Phe Ser Arg Gly Pro Leu			
	515	520	525
cgg gtc acg gtc gcg ctg cgc ccc gga ccg gtc ggc gtg ccc gag cac			2111
Arg Val Thr Val Ala Leu Arg Pro Gly Pro Val Gly Val Pro Glu His			
	530	535	540
ggg ggc ctc gtg ctc gcc tac ggc gag gtg cgc gcc ggc gcc gcc gga			2159
Gly Gly Leu Val Leu Ala Tyr Gly Glu Val Arg Ala Gly Ala Ala Gly			
	550	555	560
ctg cac ctc gac ggg ccg gga gcc gcg atc gtg cgc ctc gag			2201
Leu His Leu Asp Gly Pro Gly Ala Ala Ile Val Arg Leu Glu			
	565	570	575
tgacgcggct gggtacc			2218

<210> 33
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:SYNTHETIC

<400> 33

atgaaccgac gattcccggg ctggg

25

<210> 34

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:SYNTHETIC

<400> 34

tcactcgagg cgcacgatcg cggct

25

<210> 35

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:SYNTHETIC

<400> 35

aaatctagat gaaccgacga ttcccgggtct gggcgc

36

<210> 36

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:SYNTHETIC

<400> 36

aaaactagtt tatcactcga ggcgcacgat cgcggc

36

<210> 37

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:SYNTHETIC

<400> 37

atcgtcgggt catatttttt cctcctga

28

<210> 38

<211> 28

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence:SYNTHETIC

<400> 38

aatcaggagg aaaaaatatg aaccgacg

28

<210> 39

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:SYNTHETIC

<400> 39

aggtggttgt agacgacgtc ct

22

20